

GenCore version 4.5  
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# OM protein - protein search, using sw model

Run on: June 21, 2002, 08:25:26 ; Search time 22.96 Seconds

(without alignments)  
141.657 Million cell updates/sec

Title: US-09-351-778a-12

Sequence: 1 MTCSTIAPTDTYRNTATGL.....NEKIHRLDLKPCSLLOYD 84

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SWISSPROT\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID         | Description         |
|------------|-------|-------------|--------|------------|---------------------|
| 1          | 56    | 66.7        | 101    | E311_ADE02 | P24935 human adeno  |
| 2          | 56    | 66.7        | 101    | E311_ADE06 | O55653 human adeno  |
| 3          | 19    | 22.6        | 93     | E311_ADE05 | P17590 human adeno  |
| 4          | 6     | 7.1         | 92     | HRK_MOUSE  | P70678 mus musculi  |
| 5          | 6     | 7.1         | 121    | VMBF_POPMV | 002123 poplar mosa  |
| 6          | 6     | 7.1         | 126    | NIEW_FRASE | 002570 frankia sp.  |
| 7          | 6     | 7.1         | 136    | YRNE_CAEEL | 009420 caenorhabdl  |
| 8          | 6     | 7.1         | 142    | YB9E_YEAST | P38337 saccharomyc  |
| 9          | 6     | 7.1         | 151    | FER8_METVA | O57619 methanococc  |
| 10         | 6     | 7.1         | 152    | RK34_SPIOL | P82244 splinacia ol |
| 11         | 6     | 7.1         | 157    | HES2_MOUSE | P35429 mus musculi  |
| 12         | 6     | 7.1         | 157    | HES2_RAT   | Q93429 ratius norv  |
| 13         | 6     | 7.1         | 173    | HES2_HUMAN | P44215 haemophilus  |
| 14         | 6     | 7.1         | 184    | YEB8_HAEIN | Q93543 homo sapien  |
| 15         | 6     | 7.1         | 194    | IM22_HUMAN | Q93584 homo sapien  |
| 16         | 6     | 7.1         | 195    | NRTN_MOUSE | P97463 mus musculi  |
| 17         | 6     | 7.1         | 217    | RPE_HELPY  | Q92175 helicobacte  |
| 18         | 6     | 7.1         | 217    | RPE_HELPY  | P56188 helicobacte  |
| 19         | 6     | 7.1         | 227    | IDIL_MOUSE | P58044 mus musculi  |
| 20         | 6     | 7.1         | 240    | 45KD_TAEVO | P19697 taenia ovis  |
| 21         | 6     | 7.1         | 240    | PYRH_AQUAE | O66929 aquifex aeo  |
| 22         | 6     | 7.1         | 248    | RIBF_RHOOP | O84990 rhodococcus  |
| 23         | 6     | 7.1         | 248    | VGL2_EBV   | P03218 Epstein-ba   |
| 24         | 6     | 7.1         | 263    | V225_METVA | O57678 methanococc  |
| 25         | 6     | 7.1         | 280    | HESI_HUMAN | Q14649 homo sapien  |
| 26         | 6     | 7.1         | 281    | HESI_RAT   | O04666 ratius norv  |
| 27         | 6     | 7.1         | 282    | HESI_MOUSE | P35428 mus musculi  |
| 28         | 6     | 7.1         | 290    | HESI_CHICK | O57337 gallus gall  |
| 29         | 6     | 7.1         | 304    | PTPE_BACAM | P11029 bacillus am  |
| 30         | 6     | 7.1         | 316    | MHPF_ECOLI | P77580 escherichia  |
| 31         | 6     | 7.1         | 318    | FER8_ECOLI | P38844 saccharomyc  |
| 32         | 6     | 7.1         | 325    | YH03_YEAST | O01638 homo sapien  |
| 33         | 6     | 7.1         | 328    | IRL1_HUMAN |                     |

## ALIGNMENTS

| RESULT | ID                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | E311_ADE02 | STANDARD: | PRT: | 101 AA. |
|--------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------|-----------|------|---------|
| AC     | P24935:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |            |           |      |         |
| DT     | 01-MAR-1992 (Rel. 21, Created)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |            |           |      |         |
| DT     | 01-MAR-1992 (Rel. 21, Last sequence update)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |            |           |      |         |
| DT     | 01-DEC-1992 (Rel. 24, Last annotation update)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |            |           |      |         |
| DE     | Early E3A 11.6 kDa glycoprotein.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |            |           |      |         |
| OS     | Human adenovirus type 2.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |            |           |      |         |
| OC     | Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |            |           |      |         |
| OX     | NCBI_Taxid=10515;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |            |           |      |         |
| RN     | [1]                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |            |           |      |         |
| RP     | SEQUENCE FROM N.A.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |            |           |      |         |
| RX     | MEDLINE=81053687; PubMed=6253880;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |            |           |      |         |
| RA     | Herliase J., Courtois G., Galibert F.;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |            |           |      |         |
| RT     | "Nucleotide sequence of the Ecore D fragment of adenovirus 2 genome.";                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |            |           |      |         |
| RL     | Nucleic Acids Res. 8:2173-2192(1980).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |            |           |      |         |
| RN     | [2]                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |            |           |      |         |
| RP     | IDENTIFICATION OF PROTEIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |            |           |      |         |
| RX     | MEDLINE=93079877; PubMed=1448922;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |            |           |      |         |
| RA     | Scaria A., Tollefson A.E., Saha S.K., Wold W.S.M.;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |            |           |      |         |
| RT     | "The E3-11.6K protein of adenovirus is an Asn-glycosylated integral membrane protein that localizes to the nuclear membrane.";                                                                                                                                                                                                                                                                                                                                                                                                                                            |            |           |      |         |
| RL     | Virology 191:743-753(1992)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |            |           |      |         |
| CC     | -1- SUBCELLULAR LOCATION: INTEGRAL NUCLEAR MEMBRANE PROTEIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |            |           |      |         |
| CC     | -1- PTM: N-GLYCOSYLATED AND PROBABLY ALSO O-GLYCOSYLATED.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |            |           |      |         |
| CC     | -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER AD2 E3A 11.6 kDa, AD5 E3A 10.5 kDa, AD3 E3 9 kDa, AND AD7 E3 7.7 kDa.                                                                                                                                                                                                                                                                                                                                                                                                                                             |            |           |      |         |
| CC     | -----                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |            |           |      |         |
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| CC     | -----                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |            |           |      |         |
| DR     | EMBL: J01917; AAA92222.1;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |            |           |      |         |
| KW     | Early protein; Glycoprotein; Transmembrane.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |            |           |      |         |
| FT     | TRANSMEM 41 62                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |            |           |      |         |
| FT     | CARBOHYD 14 14                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |            |           |      |         |
| FT     | SEQUENCE 101 AA; 11644 MW; FB89FC6E921B84B CMC64;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |            |           |      |         |

Query Match 66.74; Score 56; DB 1; Length 101;  
Best Local Similarity 100.0%; Pred. No. 5.2e-53;  
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|            |            |                                                      |              |
|------------|------------|------------------------------------------------------|--------------|
| Oy         | 29         | IALMPFCIIIMWLICCKRRARPRPIYIVNPNKIHRLDGLKPCSLLOYD 84  |              |
| Db         | 46         | IALMPFCIIIMWLICCKRRARPRPIYIVNPNKIHRLDGLKPCSLLOYD 101 |              |
| RESULT     | 2          |                                                      |              |
| E311_ADE06 |            |                                                      |              |
| ID         | E311_ADE06 | STANDARD:                                            | PRT: 101 AA. |

CC 055653; 1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Early E3A 11.6 kDa glycoprotein.  
OS Human adenovirus type 6.  
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
OX NCBI\_TaxID=10334;  
RN [1]  
RA SEQUENCE FROM N.A.  
RA Reichmann H., Schaefer-Schmidt E., Geisler B., Hausmann J., Ottmann D.,  
RA Bauer U., Flunker G., Seidel W.;  
RA Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL NUCLEAR MEMBRANE PROTEIN.  
CC -1- PPM: N-GLYCOSYLATED AND PROBABLY ALSO O-GLYCOSYLATED (BY  
CC SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER AD2 E3A 11.6  
CC kDa, AD5 E3A 10.5 kDa, AD3 E3 9 kDa, AND AD7 E3 7.7 kDa.  
CC -----  
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CC -----  
CC EMBL: Y16037; CAA15991.1; Transmembrane.  
CC DR Early protein; Glycoprotein; POTENTIAL.  
CC FT TRANSMEM 41 62  
CC FT CARBOHYD 14 14 N-LINKED (GLCNAC..)(POTENTIAL).  
CC SQ SEQUENCE 101 AA; 11613 MW; EF219000939E3B4B CRC64;  
CC -----  
Query Match 66.7%; Score 56; DB 1; Length 101;  
Best Local Similarity 100.00%; Pred. No. 5; 2e-53;  
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DY 29 IALMFCVLIIMMLICCLKRRRRAPPYRPIRYIVLPHNKKIHRDGLKPSLLLOYD 84  
DB 46 IALMFCVLIIMMLICCLKRRRRAPPYRPIRYIVLPHNKKIHRDGLKPSLLLOYD 101  
-----  
RESULT 3  
AC AC E311\_ADE05 STANDARD; PRT; 93 AA.  
AC P17590;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 01-DEC-1992 (Rel. 24, Last annotation update)  
DE Early E3A 10.5 kDa glycoprotein.  
OS Human adenovirus type 5.  
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
OX NCBI\_TaxID=28285;  
RN [1]  
RA SEQUENCE FROM N.A.  
RA MEDLINE=85092388; PubMed=2981456;  
RA Cladars C., Wold S.M.;  
RA "DNA sequence of the early E3 transcription unit of adenovirus 5.";  
RL Virology 140:28-43(1985).  
RN [2]  
RP COMPLETE GENOME.  
RP MEDLINE=92087470; PubMed=1727603;  
RA Chroczek J., Bieher F., Jacot B.;  
RA "The sequence of the genome of adenovirus type 5 and its comparison  
RA with the genome of adenovirus type 2.";  
RL Virology 186:280-285(1992).  
CC -1- SUBCELLULAR LOCATION: INTEGRAL NUCLEAR MEMBRANE PROTEIN.  
CC -1- PPM: N-GLYCOSYLATED AND PROBABLY ALSO O-GLYCOSYLATED.  
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER AD2 E3A 11.6  
CC kDa, AD5 E3A 10.5 kDa, AD3 E3 9 kDa, AND AD7 E3 7.7 kDa.  
CC -----  
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[illegible]

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DB      50 KRRARP 55

RESULT  5
VMBP_POPMV STANDARD: PRT: 121 AA.
ID VMBP_POPMV 002123;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-1993 (Rel. 27, Last annotation update)
DE 14 kDa protein (Putative nucleic acid-binding protein).
OS Poplar mosaic virus (isolate ATCC PV275) (PMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
ON NCBI_TaxID=31709;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92333281; PubMed=1629709;
RA Henderson J., Glibbs M.J., Edwards M.L., Clarke V.A., Gardner K.A.,
RA Cooper J.I.;
RT "Partial nucleotide sequence of poplar mosaic virus RNA confirms its
RT classification as a Carlavirus."
RL J. Gen. Virol. 73:1887-1890(1992).
CC -1- FUNCTION: MAY ACT AS A REGULATORY FACTOR DURING VIRAL
CC TRANSCRIPTION.
CC -1- SIMILARITY: TO NUCLEIC ACID-BINDING PROTEINS FROM OTHER
CC CARLAVIRUSES.
CC -----
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CC -----
DR EMBL: X65102; CAA46227.1; -
DR EMBL: D13364; BAA02629.1; -
DR PIR: J01646; J01646.
DR PIR: S23876; S23876.
DR InterPro: IPR002568; Carla_C4.
DR Pfam: PF01623; Carla_C4; 1.
DR Zinc-finger; DNA-binding.
FT ZN_FING 62
FT SEQUENCE 121 AA; 14451 MW; 705205527BF7D3CF CRC64;
SQ

Query Match
Best Local Similarity 7.1%; Score 6; DB 1; Length 121;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 46 KRRARP 51
DB 52 KRRARP 57

RESULT 6
NIFM_FRASE STANDARD: PRT: 126 AA.
ID NIFM_FRASE 0925Y0;
AC 0925Y0;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Nitrogenase stabilizing/protective protein nifm.
ON NCBI_TaxID=47227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Euik1;
RA Chung-Sun A., Ji-Tae K., Won-Jin K., Won-Young Y.;

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RT "Nif gene organization and nucleotide sequences from Frankia Euik1
RT strain."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: May protect the nitrogenase Fe-Mo protein from oxidative
CC damage (By similarity).
CC -1- SUBUNIT: Homotrimer; associates with nifd (By similarity).
CC -1- SIMILARITY: BELONGS TO THE NIFM FAMILY.
CC -----
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CC -----
DR EMBL: AF119361; AAD17267.1; -
DR Nifrogen fixation.
KW Nitrogen fixation.
SQ SEQUENCE 126 AA; 14287 MW; 295D8C9102FD317E CRC64;

Query Match
Best Local Similarity 7.1%; Score 6; DB 1; Length 126;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 TTATGL 20
DB 80 TTATGL 85

RESULT 7
YRN6_CAEEL STANDARD: PRT: 136 AA.
ID YRN6_CAEEL 009420;
AC 009420;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Hypothetical 14.2 kDa protein R07B1.6 in chromosome X.
GN R07B1.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Rhabditidae; Caenorhabditis.
ON NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Kershaw J.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: Z48621; CAA8543.1; -
DR Wormpep: R07B1.6; CE01632.
DR InterPro: IPR002601; C6.
DR Pfam: PF01681; C6; 1.
KW Hypothetical protein.
SQ SEQUENCE 136 AA; 14169 MW; D7F47A83F3F81787 CRC64;

Query Match
Best Local Similarity 7.1%; Score 6; DB 1; Length 136;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TTAFTT 10
DB 31 TTAFTT 36

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RESULT 8
RT YB9E_YEAST STANDARD: PRT: 142 AA.
AC P38337:
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Hypothetical 16.4 kDa protein in POP4-SHM1 Intergenic region.
GN YB8258C OR YB81726.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=93220397; PubMed=8465606;
RA Dolignon F., Bileau N., Crouzet M., Aigle M.;
RT "The complete sequence of a 19,482 bp segment located on the right
RL arm of chromosome II from Saccharomyces cerevisiae.";
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CC -----
CC EMBL: X70529; CAA49922.1;
CC EMBL: Z36127; CAA85221.1;
CC PIR: S32960; S32960
CC SGD: S0000462; YBR258C.
CC Hypothetical protein.
SQ SEQUENCE 142 AA; 16429 MW; 12E73FC3D2D25D7 CRC64;

Query Match 7.1%; Score 6; DB 1; Length 142;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 GLUTAL 24
DB 71 GLUTAL 76

RESULT 9
RT FER8_METJA STANDARD: PRT: 151 AA.
AC Q57619;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative ferredoxin M0155.
GN M0155.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kettleberg A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
RA Uitterlbeck T.R., Kelley J.M., Peterson J.D., Sedow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kalne B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

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RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073(1996).
CC -1- COFACTOR: BINDS 1 4FE-4S CLUSTER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL TYPE FERREDOXIN FAMILY.
CC -----
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CC -----
CC EMBL: U67472; AAB98137.1;
CC HSP: P00195; 1CLF.
CC TIGR: M0155;
DR InterPro: IPR001450; 4FE4S-ferredoxin.
DR Pfam: PF00037; fer4.1.
DR PRINTS: PR00353; 4FE4S-FERREDOXIN.
DR PROSITE: PS00198; 4FE4S-FERREDOXIN; 1.
KM Hypothetical protein; Electron transport; 4Fe-4S; Iron-sulfur;
KM Complete proteome.
FT METAL 73 73 IRON-SULFUR (4FE-4S) (POTENTIAL).
FT METAL 76 76 IRON-SULFUR (4FE-4S) (POTENTIAL).
FT METAL 79 79 IRON-SULFUR (4FE-4S) (POTENTIAL).
FT METAL 82 83 IRON-SULFUR (4FE-4S) (POTENTIAL).
SQ SEQUENCE 151 AA; 16985 MW; 86EC9B27DEFAEAF1 CRC64;

Query Match 7.1%; Score 6; DB 1; Length 151;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 58 IIVLNP 63
DB 5 IIVLNP 10

RESULT 10
RT RK34_SPIOI STANDARD: PRT: 152 AA.
AC P82244;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 50S ribosomal protein L34, chloroplast precursor.
GN RPL34.
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE FROM N.A.; SEQUENCE OF 92-101, AND MASS SPECTROMETRY.
RC STRAIN=CV, ALMARO; TISSUE=Leaf;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamauchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -1- PUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- TISSUE SPECIFICITY: UBQUITOUS.
CC -1- MASS SPECTROMETRY: MW=6767.1; METHOD=Electrospray; RANGE=92-152.
CC -1- SIMILARITY: BELONGS TO THE L34P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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 CC EMBL: AF238221; AAF64157.1; -  
 DR InterPro: IPR000771; Ribosomal\_L34.  
 DR Pfam: PF00468; Ribosomal\_L34; 1.  
 DR PROSITE: PS00784; RIBOSOMAL\_L34; FALSE\_NEG.  
 KM Ribosomal protein; Chloroplast; Transit peptide; rRNA-binding.  
 FT TRANSIT 1 91  
 FT CHAIN 92 152  
 FT SEQUENCE 152 AA; 16095 MW; 755A990D441ADB18 CRC64.

Query Match 7.18; Score 6; DB 1; Length 152;  
 Best Local Similarity 100.0%; Pred. No. 33;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 45 LKRRRA 50  
 |||||  
 Db 127 LKRRRA 132

RESULT 11  
 HES2\_MOUSE  
 ID HES2\_MOUSE STANDARD; PRT; 157 AA.  
 AC 054792;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Transcription factor HES-2 (Hairy and enhancer of split 2).  
 GN HES2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/J;  
 RX MEDLINE=98234545; PubMed=9570950;  
 RA Nishimura M., Isaka F., Ishibashi M., Tomita K., Tsuda H.,  
 RA Nakanishi S., Kageyama R.;  
 RT Structure, chromosomal locus, and promoter of mouse Hes2 gene, a  
 RT homologue of Drosophila hairy and enhancer of split.;  
 RL Genomics 49:69-75(1998).  
 CC -1- FUNCTION: TRANSCRIPTIONAL REPRESSOR OF GENES THAT REQUIRE A BHLH  
 CC PROTEIN FOR THEIR TRANSCRIPTION.  
 CC -1- SUBUNIT: TRANSCRIPTION REPRESSION REQUIRES FORMATION OF A COMPLEX  
 CC WITH A CO-REPRESSOR PROTEIN (GROUCHO).  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- DOMAIN: HAS A PARTICULAR TYPE OF BASIC DOMAIN (PRESENCE OF A  
 CC HELIX-INTERRUPTING PROLINE) THAT BINDS TO THE N-BOX (CACNAG).  
 CC RATHER THAN THE CANONICAL E-BOX (CANNTG).  
 CC -1- DOMAIN: THE CARBOXYL-TERMINAL WRPW MOTIF IS A TRANSCRIPTIONAL  
 CC REPRESSION DOMAIN NECESSARY FOR THE INTERACTION WITH GROUCHO. A  
 CC TRANSCRIPTIONAL CO-REPRESSOR RECRUITED TO SPECIFIC TARGET DNA BY  
 CC HAIRY-RELATED PROTEINS.  
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF  
 CC TRANSCRIPTION FACTORS. "HAIRY" SUBFAMILY.  
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 CC -----  
 DR EMBL: AB009967; BAA24091.1; -  
 DR MGD: MGI:1098624; Hes2.  
 DR InterPro: IPR001015; HLH\_MYC.  
 DR InterPro: IPR001092; HLH\_dlm.  
 DR InterPro: IPR003650; Orange.  
 DR Pfam: PF00010; HLH; 1.  
 DR SMART: SM00353; HLH; 1.

DR SMART: SM00511; ORANGE; 1.  
 DR PROSITE: PS00038; HELIX\_LOOP\_HELIX; 1.  
 KM Transcription regulation; DNA-binding; Nuclear protein; Repressor.  
 FT DNA\_BIND 13 26  
 FT BASIC DOMAIN.  
 FT TRANSIT 27 71  
 FT HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).  
 FT DOMAIN 139 148  
 FT PRO-RICH.  
 FT WRPW MOTIF (REQUIRED FOR ACTIVITY)  
 FT DOMAIN 154 157  
 FT (BY SIMILARITY).  
 FT SEQUENCE 157 AA; 17231 MW; 570A0C67F4992EA7 CRC64.

Query Match 7.18; Score 6; DB 1; Length 157;  
 Best Local Similarity 100.0%; Pred. No. 34;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 46 KRRRAR 51  
 |||||  
 Db 23 KRRRAR 28

RESULT 12  
 HES2\_RAT  
 ID HES2\_RAT STANDARD; PRT; 157 AA.  
 AC P35429;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Transcription factor HES-2 (Hairy and enhancer of split 2).  
 GN HES2 OR HES-2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryonic brain;  
 RX MEDLINE=93358886; PubMed=8354270;  
 RA Ishibashi M., Sasai Y., Nakanishi S., Kageyama R.;  
 RT "Molecular characterization of HES-2, a mammalian helix-loop-helix  
 RT factor structurally related to Drosophila hairy and enhancer of  
 RT split.";  
 RL Eur. J. Biochem. 215:645-652(1993).  
 CC -1- FUNCTION: TRANSCRIPTIONAL REPRESSOR OF GENES THAT REQUIRE A BHLH  
 CC PROTEIN FOR THEIR TRANSCRIPTION.  
 CC -1- SUBUNIT: TRANSCRIPTION REPRESSION REQUIRES FORMATION OF A COMPLEX  
 CC WITH A CO-REPRESSOR PROTEIN (GROUCHO).  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- DOMAIN: HAS A PARTICULAR TYPE OF BASIC DOMAIN (PRESENCE OF A  
 CC HELIX-INTERRUPTING PROLINE) THAT BINDS TO THE N-BOX (CACNAG).  
 CC RATHER THAN THE CANONICAL E-BOX (CANNTG).  
 CC -1- DOMAIN: THE CARBOXYL-TERMINAL WRPW MOTIF IS A TRANSCRIPTIONAL  
 CC REPRESSION DOMAIN NECESSARY FOR THE INTERACTION WITH GROUCHO. A  
 CC TRANSCRIPTIONAL CO-REPRESSOR RECRUITED TO SPECIFIC TARGET DNA BY  
 CC HAIRY-RELATED PROTEINS.  
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF  
 CC TRANSCRIPTION FACTORS. "HAIRY" SUBFAMILY.  
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 CC -----  
 DR EMBL: D14029; BAA03118.1; -  
 DR PIR: S35037; S35037.  
 DR TRANSFAC: T01650; -  
 DR InterPro: IPR001015; HLH\_MYC.  
 DR InterPro: IPR001092; HLH\_dlm.  
 DR InterPro: IPR003650; Orange.  
 DR Pfam: PF00010; HLH; 1.  
 DR SMART: SM00353; HLH; 1.

DR SMART: SM00511: ORANGE: 1.  
 DR PROSITE: PS00038: HELIX\_LOOP\_HELIX: 1.  
 KW Transcription regulation: DNA-binding: Nuclear protein: Repressor.  
 FT DNA\_BIND 13 26 BASIC DOMAIN.  
 FT DOMAIN 27 71 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).  
 FT DOMAIN 139 148 PRO-RICH.  
 FT DOMAIN 154 157 WRPW MOTIF (REQUIRED FOR ACTIVITY)  
 (BY SIMILARITY)  
 FT SEQUENCE 157 AA: 17028 MW: B5D621E814AE0369 CRC64:

Query Match 7.1%; Score 6; DB 1; Length 157;  
 Best Local Similarity 100.0%; Pred. No. 34;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 46 KRRRAR 51  
 |||||  
 DB 23 KRRRAR 28

RESULT 13  
 HES2\_HUMAN STANDARD: PRT; 173 AA.  
 AC 09Y543: 09Y542:  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Transcription factor HES-2 (Hairy and enhancer of split 2).  
 GN HES2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Howden P.;  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: TRANSCRIPTIONAL REPRESSOR OF GENES THAT REQUIRE A BHLH  
 CC PROTEIN FOR THEIR TRANSCRIPTION (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Nuclear (BY SIMILARITY).  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2; MAY BE  
 CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- DOMAIN: HAS A PARTICULAR TYPE OF BASIC DOMAIN (PRESENCE OF A  
 CC HELIX-INTERUPTING PROLINE) THAT BINDS TO THE N-BOX (CACNAG),  
 CC RATHER THAN THE CANONICAL E-BOX (CANNTG).  
 CC -1- DOMAIN: THE CARBOXYL-TERMINAL WRPW MOTIF IS A TRANSCRIPTIONAL  
 CC REPRESSION DOMAIN NECESSARY FOR THE INTERACTION WITH GRCUCHO, A  
 CC TRANSCRIPTIONAL CO-REPRESSOR RECRUITED TO SPECIFIC TARGET DNA BY  
 CC HAIRY-RELATED PROTEINS (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF  
 CC TRANSCRIPTION FACTORS. "HAIRY" SUBFAMILY.

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CC EMBL: AL031848: CAB46198.1; ..  
 DR EMBL: AL031848: CAB46199.1; ..  
 DR InterPro: IPR003015: HLH\_MYC.  
 DR InterPro: IPR001092: HLH\_dim.  
 DR InterPro: IPR003650: Orange.  
 DR Pfam: PF00010: HLH: 1.  
 DR SMART: SM00511: ORANGE: 1.  
 DR PROSITE: PS00038: HELIX\_LOOP\_HELIX: 1.  
 KW Transcription regulation: DNA-binding: Nuclear protein: Repressor;  
 KW Alternative splicing.  
 FT DNA\_BIND 13 26 BASIC DOMAIN.  
 FT DOMAIN 27 71 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).

FT DOMAIN 139 167 PRO-RICH.  
 FT DOMAIN 170 173 WRPW MOTIF (REQUIRED FOR ACTIVITY)  
 (BY SIMILARITY).  
 FT VARSPIC 48 173 NSNCSKLEKADVLEMTVFLELPASSWPTAAPPCDSYRE  
 GYSACVRLARLVPCRVLEPAPASRLLEMRPAASATLD  
 GGRAGDSGSPASAPAPAPASAPAPAPSPSPSPCGFLM  
 RPW -> DASGHWHTPLHAQNCFLYIQAEQPPA (IN  
 ISOFORM 2)  
 FT SEQUENCE 173 AA: 18470 MW: B3751F4576B84F3D CRC64:

Query Match 7.1%; Score 6; DB 1; Length 173;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 46 KRRRAR 51  
 |||||  
 DB 23 KRRRAR 28

RESULT 14  
 YE89\_HAEIN STANDARD: PRT; 184 AA.  
 ID YE89\_HAEIN  
 AC P44215;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein H11489.  
 GN H11489.  
 OS Haemophilus influenzae.  
 CC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
 CC Haemophilus.  
 OX NCBI\_TaxID=727;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=RD / KW20 / ATCC 51907;  
 RC MEDLINE=95350630; PubMed=7542800;  
 RX Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
 RA Kellavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
 RA McInerney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,  
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,  
 RA Uretchback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
 RA Fine L.D., Fritchman J.L., Fuhmann J.L., Geoghegan N.S.M.,  
 RA Gnehm C.U., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
 RA Venter J.C.;  
 RT "Whole-genome random sequencing and assembly of Haemophilus  
 RT influenzae Rd.";  
 RL Science 269:496-512(1995).

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CC EMBL: U13826: AAC3143.1; ..  
 DR TIGR: H11489;  
 KW Hypothetical protein: Complete proteome.  
 SQ SEQUENCE 184 AA: 20782 MW: C298357DBED80211 CRC64;

Query Match 7.1%; Score 6; DB 1; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 76 PCSLL 81  
 |||||  
 DB 73 PCSLL 78

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RESULT 15
IM22_HUMAN STANDARD: PRT; 194 AA.
ID IM22_HUMAN
AC O9Y584;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mitochondrial import inner membrane translocase subunit TIM22.
GN TIM22 OR TIM22.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N. A.
RA Bauer M.F., Brunner M., Neupert W., Gerblitz K.-D., Hofmann S.;
RT Cloning and mapping of human Tim22, homologous to S.cerevisiae Tim22,
RT a membrane-integrated component of the Tim22-54 machinery for the
RT import of mitochondrial carrier proteins..";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ESSENTIAL COMPONENT OF MITOCHONDRIAL INNER MEMBRANE
CC PROTEIN IMPORT PATHWAY. INVOLVED IN THE IMPORT OF PROTEINS
CC TARGETED TO THE INNER MEMBRANE OF THE MITOCHONDRION SUCH AS
CC MITOCHONDRIAL CARRIER FAMILY MEMBERS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TIM17/TIM22/TIM23 FAMILY.
CC -----
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CC -----
DR EMBL; AE155330; AAD40106.1; -.
DR InterPro; IPR003397; Tim17. 1.
DR Pfam; PF02466; Tim17. 1.
KM Protein transport; Transmembrane; Mitochondrion; Inner membrane.
FT TRANSMEM 74 94 POTENTIAL.
FT TRANSMEM 123 143 POTENTIAL.
FT TRANSMEM 170 190 POTENTIAL.
SQ SEQUENCE 194 AA: 20270 MW: DC986E23DDF18377 CRC64;

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Query Match 7.1%; Score 6; DB 1; Length 194;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 78 SULLOY 83
DB 26 SULLOY 31

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Job time: 311 sec

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